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Urine metabolic profile in rheumatoid arthritis development

Schrader de Oliveira, Marianne; Bartikoski, Barbara; de Souza Silva, Jordana; Cavalheiro do Espirito Santo, Rafaela; Young, Stephen; Xavier, Ricardo

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Urine Metabolic Profiles in Rheumatoid Arthritis Development

Marianne Schrader de Oliveira, Paulo Vinicius Alabarse, Rafaela Cavalheiro, Stephen Peter Young, Ricardo Machado Xavier

Abstract

Introduction: Rheumatoid arthritis (RA) is a chronic inflammatory disease characterized by increased mortality and associated with metabolic disorders including dyslipidaemia, insulin resistance and cachexia. Since the metabolomic profile is known to vary in response to different inflammatory conditions, those metabolite analysis could substantially improve diagnosis and prognosis.

Objective: To analyses the urine metabolic profile and assess to its correlation with body composition parameters and disease activity of RA patients.

Methods: Seventy-nine RA patients, according to ACR/EULAR 2010 classification criteria, aged between 40 and 70 years, were recruited and followed for 12 months. Disease activity, body composition, fatigue and urine metabolome were measured. Body composition was assessed by total body dual-energy x-ray absorptiometry (DXA) for measurement of appendicular lean mass index (ALMI). Disease activity was assessed by Disease Activity Score-28 (DAS28) with erythrocyte sedimentation rate (ESR). Fatigue as assessed by the Functional Assessment of Chronic Illness Therapy (FACIT). Nuclear Magnetic Ressonance (NMR) spectroscopy measurements were performed to evaluate the profile of metabolic changes during the disease development, resulting in the identification of 48 metabolites in urine collected at the baseline and after one year after. Frequency analysis, Pearson Correlation and Multivariate data analysis with orthogonal projections to latent structures (OPLS) method were performed and a statistical significance was considered as $p<0.05$.

Results: The study population was characterized by the majority of women (86.7%), mean age 56 years old, around 80% with anti-CPP and Rheumatoid Factor reagent. During the one year of follow-up, there was no huge substantial variation in the DAS28 measurement (baseline: 3,8, after 12 months: 4,0). It is By for this reason, we belivebelieve that we could not find any significant correlation between the metabolome pattern and DAS28 score ($p>0.05$). However, Tthere was a significant increase of methyl-histidine, creatinine, L-serine and urea by during the development of the disease, metabolites that are involved in the muscular muscle-related metabolismconstitutions pathways. . Fatigue was positively correlated with L-serine/creatinine (r: - 0,4, $p<0.001$). Appendicular lean mass index (ALMI) also presented showed a difference when which correlated to with the increase of urea and creatinine (r: 0,3, $p<0.019$).

Conclusion: The potential biomarkers indicated that the RA metabolic disturbance might be associated with inflammation, injury, fatigue and amino acid metabolism. Those These findings suggest that urine metabolome analysis may be an interesting approach to monitoring rheumatological disease related

to muscle changes and fatigue, which are of major concern to patients, and this ~~that~~ could be ~~more~~ further explored in future ~~trials~~studies.